

GenCore version 4.5  
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UM protein - protein search, using sw model

Run on: November 5, 2001, 13:02:37 ; Search time 100.35 Seconds

(With out alignments)  
486,503 Million cell updates/sec

Title: US-09-593-316-2

Perfect score: 2003

Sequence: 1 MANKGKVLISMLVSTIVV.....IKLYKMSQIKRYVNNV 369

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 13230527 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1711.5	85.4	376	6 Q28855
2	677	33.8	274	4 Q90065
3	673	33.6	274	4 Q90068
4	673	33.6	295	4 Q15951
5	673	33.6	354	4 Q14490
6	671	33.5	274	4 Q90063
7	670	33.4	274	4 Q14758
8	670	33.4	274	4 Q90069
9	670	33.4	274	4 Q90181
10	667	33.3	274	6 Q91T12
11	667	33.3	274	6 Q91T12
12	665	33.2	274	4 Q90067
13	665	33.2	274	4 Q90062
14	664	33.2	274	4 Q90066
15	664	33.1	274	6 Q91T15
16	662	33.1	274	4 Q90064
17	661	33.0	274	4 Q15512
18	660	33.0	274	6 Q91T13
19	660	33.0	274	6 Q18825

20	658	32.9	274	6 Q97549
21	656	32.8	348	11 Q9ET32
22	655	32.7	312	6 Q9T1N4
23	649	32.4	277	6 Q9TSM1
24	649	32.4	289	6 Q9TUP0
25	646	32.3	327	11 Q9EOW3
26	646	32.3	332	11 Q9EOW2
27	645.5	32.2	271	6 Q9TV74
28	643	32.1	348	6 Q9TUD9
29	639	31.9	347	4 Q90K15
30	629.5	31.4	262	6 Q9FTN3
31	628.5	31.4	309	6 Q97551
32	627	31.3	347	6 Q95156
33	612	30.6	364	6 Q77563
34	538.5	26.9	229	4 Q9NW01
35	537.5	26.8	229	4 Q99479
36	532.5	26.6	229	4 Q9NM02
37	489.5	24.4	209	6 Q9GM53
38	468.5	23.4	190	6 Q62752
39	468.5	23.4	190	6 Q62858
40	467.5	23.3	190	6 Q62751
41	467.5	23.3	190	6 Q62753
42	464.5	23.2	190	6 Q62749
43	464.5	23.2	190	6 Q62748
44	460.5	23.0	209	6 Q9GM54
45	450.5	22.5	186	6 Q62750

## ALIGNMENTS

RESULT 1  
ID Q28855 PRELIMINARY: PRT: 376 AA.  
AC Q28855:  
DT 01-FEB-1997 (TRENBLER, 02, created)  
DT 01-FEB-1997 (TRENBLER, 02, last sequence update)  
DT 01-OCT-2000 (TRENBLER, 15, last annotation update)  
DE ALPHA 1.3 GALACTOSYLTRANSFERASE.  
OS PLYTHRINI (New World monkeys).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates.  
OX NCBI\_TaxID=9479;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9431837; PubMed=8054718;  
RA Henion T.R., Macher B.A., Anuraki F., Gallili U.;  
RT "Defining the minimal size of catalytically active primate alpha 1.3  
RT galactosyltransferase: structure-function studies on the recombinant  
RT truncated enzyme.";  
RL Glycobiology 4:193-201(1994).  
DR EMBL: S71333; AAB31587.2; -.  
SO SEQUENCE 376 AA; 44471 MW; 13C490C0BF2FAZDF CRC64;

Query Match 85.4%; Score 1711.5; DB 6; Length 376;  
Best local Similarity 83.0%; Pred. No. 4,1e-130;  
Matches 313; Conservative 33; Mismatches 22; Indels 9; Gaps 4;

QY 1 MANKGKVLISMLVSTIVVFMFYIHSPESSLPWINSRNPFSGSSNLUKEMWPRMTN 60  
DB 1 MANKGKVLISMLVSTIVVFMFYIHSPESSLPWINSRNPFSGSSNLUKEMWPRMTN 59  
QY 61 NG---VOEEDVDVDEK---EQRKE-DKSKRLSDMFNPKRPEVVMIMAKAPVWMT 112  
DB 60 NGHNHVOQFEEDFDKEGREGDEOKKENDTFLPLMFMNKKRPEVMTYQKAPAPVWMT 119  
QY 113 TYNRAVLDDYAAKOKITVGLTFAVGRYIEHYLEELTSANKRPMGGRVITYVWVWS 172  
DB 120 TYNKAILEENYAAKOKITVGLTFAVGRYIEHYLEELTSANKRPMGGRVITYVWVWS 179  
QY 173 RMLPELGRPSKRVPEVKRERRMQVSWVRMKTIGEHVANIQRVDFLCMDVQVQV 242  
DB 172 RMLPELGRPSKRVPEVKRERRMQVSWVRMKTIGEHVANIQRVDFLCMDVQVQV 242

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DB 180 KAFVLEHLMRSEKFEVKEVKEKRWOLDSMKMKITIGENHLLAHLEHVDLPTCMWVQVFO 239
GY 233 DEGEVETTESVAOLQAWMYKADPEFEYERKESAAVTPGEGDPYHAAIFGGTPTGV 292
DB 240 HDPVGTALQNSVAOLQAWMYKADPEFEYERKESAAVTPGEGDPYHAAIFGGTPTGV 299
GY 293 LNTLOTFKGTLLKDKKNLLEAGWHDHSHLNKFFLNKPTKLLSPKCYWYHIGLPADIKL 352
DB 300 LNTLOTFKGTLLKDKKNLLEAGWHDHSHLNKFFLNKPTKLLSPKCYWYHIGLPADIKL 359
GY 453 VKKSWQTKRYNNVNNV 469
DB 460 VKKSWQTKRYNNVNNV 476

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## RESULT 2

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ID Q99065 PRELIMINARY PRT 274 AA.

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AC Q99065
DE 01 MAY 2000 (TREMUR01, 13, created)
DE 01 MAY 2000 (TREMUR01, 13, last sequence update)
DE 01 MAY 2000 (TREMUR01, 13, last annotation update)
DE C1S AB SPECIFIC ALPHA 1-3 N-ACETYLGLACTOSAMINYLTRANSFERASE
DE (FRAGMENT).
GN APO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto F.;
RT "Human histo blood group ABO gene locus alleles."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF144428; AAD26580.1; J.
DR EMBL: AF144427; AAD26580.1; JOINED.
DR Trastoraso.
KW NON_TER
FT NON_TER 274
FT SEQUENCE 274 AA; 51991 MW; F78E6270528E2955 CRC64;

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Query Match 33.8%; Score 677; DB 4; Length 274;
Best local similarity 47.1%; Pred. No. 6.7e-47;
Matches 129; Conservative 49; Mismatches 94; Indels 2; Gaps 2;

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GY 95 REEVYIMDKKAPVWVESTYNNRAVLDVYAKKLTGCTLVFAWGRVLEHYLEETLSANK 154
DB 1 KRDVAVTPMLAPLVWGTENFDLNEQFRIGNTTIGLVATARKYVA-FLKLETFEAK 59
GY 155 HFWGHVATFEVWVNDVSRMLLELAPLRSKFEVKEVKEKRWQDSVNRKKTIGENHVAH 214
DB 60 HFWGHVATFEVWVNDVSRMLLELAPLRSKFEVKEVKEKRWQDSVNRKKTIGENHVAH 119
GY 215 TGRVDFLECMVNDVQVGFETLAGESVAOLQAWMYKADPEFEYERKESAAVTPG 274
DB 120 TGRVDFLECMVNDVQVGFETLAGESVAOLQAWMYKADPEFEYERKESAAVTPG 179
GY 275 EGGFYVDAIFGGTPTGVNTLOTFKGTLLKDKKNLLEAGWHDHSHLNKFFLNKPTKLL 344
DB 180 EGGFYVDAIFGGTPTGVNTLOTFKGTLLKDKKNLLEAGWHDHSHLNKFFLNKPTKLL 239
GY 345 SPEKCYWYHIGLPADIKLVKMSWQTKRYNNVNN 367
DB 240 SPEKCYWYHIGLPADIKLVKMSWQTKRYNNVNN 273

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RESULT 3
ID Q99068 PRELIMINARY PRT 274 AA.
AC Q99068
DE 01 MAY 2000 (TREMUR01, 13, created)
DE 01 MAY 2000 (TREMUR01, 13, last sequence update)

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DE 01-MAY-2000 (TREMUR01, 13, last annotation update)
DE A1-SPECIFIC ALPHA 1-3 N-ACETYLGLACTOSAMINYLTTRANSFERASE (FRAGMENT).
GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto F.;
RT "Human histo-blood group ABO gene locus alleles."
RL Submitted (MAR 1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF144419; AAD26576.1; JOINED.
DR Trastoraso.
KW NON_TER
FT NON_TER 274
FT SEQUENCE 274 AA; 51977 MW; 71E9047A648E2DBA CRC64;

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Query Match 33.6%; Score 673; DB 4; Length 274;
Best local similarity 46.7%; Pred. No. 1.4e-46;
Matches 128; Conservative 49; Mismatches 95; Indels 2; Gaps 2;

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GY 95 REEVYIMDKKAPVWVESTYNNRAVLDVYAKKLTGCTLVFAWGRVLEHYLEETLSANK 154
DB 1 KRDVAVTPMLAPLVWGTENFDLNEQFRIGNTTIGLVATARKYVA-FLKLETFEAK 59
GY 155 HFWGHVATFEVWVNDVSRMLLELAPLRSKFEVKEVKEKRWQDSVNRKKTIGENHVAH 214
DB 60 HFWGHVATFEVWVNDVSRMLLELAPLRSKFEVKEVKEKRWQDSVNRKKTIGENHVAH 119
GY 215 TGRVDFLECMVNDVQVGFETLAGESVAOLQAWMYKADPEFEYERKESAAVTPG 274
DB 120 TGRVDFLECMVNDVQVGFETLAGESVAOLQAWMYKADPEFEYERKESAAVTPG 179
GY 275 EGGFYVDAIFGGTPTGVNTLOTFKGTLLKDKKNLLEAGWHDHSHLNKFFLNKPTKLL 344
DB 180 EGGFYVDAIFGGTPTGVNTLOTFKGTLLKDKKNLLEAGWHDHSHLNKFFLNKPTKLL 239
GY 345 SPEKCYWYHIGLPADIKLVKMSWQTKRYNNVNN 367
DB 240 SPEKCYWYHIGLPADIKLVKMSWQTKRYNNVNN 273

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## RESULT 4

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ID Q15951 PRELIMINARY PRT 295 AA.
AC Q15951;

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DE 01-MAY-1996 (TREMUR01, 01, created)
DE 01-JAN-1999 (TREMUR01, 09, last sequence update)
DE 01-NOV-1999 (TREMUR01, 12, last annotation update)
DE HISTO-BLOOD GROUP A2 TRANSFERASE (FRAGMENT).
GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:92392351; PubMed 1520422;
RA Yamamoto F.; McNoll J.D.; Hakomori S.;
RT "Human histo-blood group A2 transferase coded by A2 allele, one of the
RT A subtypes, is characterized by a single base deletion in the coding
RT sequence, which results in an additional domain at the catalytic
RT terminal."
RT Biochem. Biophys. Res. Commun. 187:366-374 (1992).

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GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto F.;
RT "Human histo-blood group ABO gene locus alleles."
RL Submitted (MAR 1999) to the EMBL/GenBank/DBJ databases.
EMBL: S44054; AAB2167.1;

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[illegible][illegible]

Query Match 33.4%; Score 670; DB 4; Length 274;

Best Local Similarity 46.4%; Pred. No. 2.5e-46; Matches 127; Conservative 49; Mismatches 96; Indels 2; Gaps 2;

95 RPEVNTMTDKKAPVWEGYVKNRAVLDDYAKOKITGLTFVAVGRYTEHLEFLTSANK 154

1 KKVLYVTPMLAPLWEGITFINIDILNEQFLQNTTIGLTFALAKKYVA-FLKLEFLTAEK 59

155 HFVNGHVRIFYVWVDVSRMPLLELPLRSFKVEVKKPERKMODVSNVRKKTIGEIVAH 214

60 HFVNGHVRIFYVETDQAAVAVRYLTIGRQLSVLEVAKYKRMQDVSRKRMEMISDFCGR 119

215 IQREVDPLFCMDVDVQVQDEFGVETLGEVSAQIQAMWYKADPDEFTYERKRESAAVTPFG 274

120 FLSEVDYLVCVDVDMERDVGVEILTPLFGTLHPFGYSSREAFYTERRPOSOAVTPKD 179

275 EGDYVYHAALFEGGTPVNLITGECFKGLDKKNDLEAQWHDHSHLNKRYFLNKPRTIL 334

180 EGDYVYIGGFGGSGVQEVQRLTRACHQAMVDAQNGIEAVWHDHSHLNKRYFLNKPRTIL 239

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

240 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 273

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367

287 SPEYLMQDQLGMPAVLRKLRFAVPRKNQAVRN 320

335 SPEYCMQDYN-IGLPADIKLVKMSWQTEYNNVRN 367



DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DE 01-MAY-2000 (TREMBLrel. 13, last annotation update)  
 DE ABO GLYCOSYLTRANSFERASE (FRAGMENT).  
 CN MAMU\_ABO.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecidae; Macaca.  
 OX NCBI\_TaxId=9544;  
 KN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RH427;  
 RX MEDLINE=99409815; PubMed=10480696;  
 RA Kernatrec N., Koudinet F., Apoll P.A., Blancher A.;  
 RT "Comparison of allele O sequences of the human and non-human primate  
 ABO system.";  
 RL Immunogenetics 49:517-526(1999).  
 DR EMBL: AF094693; AAD56308.1; -;  
 DR EMBL: AF094692; AAD56308.1; JOINED.  
 KW Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 274 AA: 31905 MW: 1038634615E5F8E6 CRC64;

Query Match 33.1%; Score 663; DB 6; Length 274;

Best Local Similarity 46.7%; Pred. No. 9e-46; Mismatches 98; Indels 2; Gaps 2;

QY 95 KREVVTIMKKAPEVVECTYNRAVLDDVYAKOKITVGLTFVAVGRYTEHYLLEELTSANK 154  
 DB 1 KRDVLVTPMLAPLIVEGTFNIDLNQFLQNTTIGLTFPAIKKYVA-FLKLFLETAEK 59  
 QY 155 HEMVGRVLFYVWVDVSRMPLIEGLPSKFEVFEVKKPERRWQDVSMVRKKTIGEHVAH 214  
 DB 60 HEMVGRVHYVFTDQPAVPAVALQTGRQLSYLVRAVYKRWQDVSMRRMEMISDFCERR 119  
 QY 215 LQREVDFLECMQDVQVDFQDFGVETLGSVAQLQAMWYKADDPFTYERKRKSAATPEG 274  
 DB 120 FLESEVDYLCADMDMEFRQVGVETLPLEGLHPAFVGSSEAFYERKRPOSQATPKD 179  
 QY 275 EGIIFYHAAIFGSIPTQVINIIOPECKGILDKKNDIEAQMHDESHLNKYFLNKPTKIL 334  
 DB 180 EGDIFYMGAFPGSSVQVQRLTRACHQAMVDAQNSTEAVWHDESHLNKYLRLHKPTKYL 239  
 QY 335 SPEYCMQVH-IGLPADIKLKKMSWDTKEYNVVN 367  
 DB 240 SPEYIMDQOILGMPAVLRKLRFAVAPKRNQAVRN 273

Search completed: November 5, 2001, 15:22:20  
 Job time: 8183 sec

